

09/869142

SEQUENCE LISTING

JC03 Rec'd PCT/PTC 26 JUN 2001

<110> SHOWA DENKO K.K.

<120> NOVEL RHODOCOCCLUS BACTERIA, NITRILASE GENE, NITRYL HYDRATASE GENE AND
AMIDASE GENE FROM RHODOCOCCLUS BACTERIUM, AND PROCESS FOR PRODUCING CARBOXYLIC
ACIDS USING THEM

<130> Q64574

<150> USSN 60/183,754

<151> 2000-02-22

<150> USSN 60/183,821

<151> 2000-02-22

<150> JPA 2000-107855

<151> 2000-04-10

<150> JPA 2000-021797

<151> 2000-01-26

<150> JPA 11-303212

<151> 1999-10-26

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<170> PatentIn version 3.1

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85

90

95

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Ser Leu Asn Phe Asn Gln Arg Arg Thr Thr Pro Val Asn Thr Pro Leu
 305 310 315 320

Ser Thr Ile His Ala Thr His Thr Phe Val Pro Gln Phe Gly Ala Leu

Filed: June 26, 2001

Inventor: E. Kramer

202-293-7060

Sequence Listing

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Arg Lys Phe Asp Pro Ala Glu Ile Glu Lys Ala Ile Glu Arg Leu His
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175

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gta cgc cga ctg ctc gac gcc ggc gca acc atc acc ggc aaa gcg gtg	1513
Val Arg Arg Leu Leu Asp Ala Gly Ala Thr Ile Thr Gly Lys Ala Val	
125 130 135 140	

tgc gaa gat ctc tgc ttc tcc ggc gcc agc ttc act tcc cac ccc cag	1561
Cys Glu Asp Leu Cys Phe Ser Gly Ala Ser Phe Thr Ser His Pro Gln	
145 150 155	
ccg gtc cgc aac ccc tgg gac gaa agc cgc atc acc ggc ggc tcg tcc	1609
Pro Val Arg Asn Pro Trp Asp Glu Ser Arg Ile Thr Gly Gly Ser Ser	
160 165 170	
agc ggc agc ggc gcc ctg gtc gcc agc ggc cag gtg gat atg gca gtc	1657
Ser Gly Ser Gly Ala Leu Val Ala Ser Gly Gln Val Asp Met Ala Val	
175 180 185	
ggc ggc gac cag ggc ggt tcg atc cgc atc ccc gcc gcg ttc tgc ggc	1705
Gly Gly Asp Gln Gly Gly Ser Ile Arg Ile Pro Ala Ala Phe Cys Gly	
190 195 200	
atc gtc gga cac aaa ccc acc cac gga ctg gtc ccc tat acg gga gca	1753
Ile Val Gly His Lys Pro Thr His Gly Leu Val Pro Tyr Thr Gly Ala	
205 210 215 220	
ttt ccc atc gaa cga acc atc gac cac ctc ggt ccg atg acg cgc acg	1801
Phe Pro Ile Glu Arg Thr Ile Asp His Leu Gly Pro Met Thr Arg Thr	
225 230 235	
gtc agc gac gcc gcc gca atg ctc acc gtc ctc gcc ggc acc gac ggc	1849
Val Ser Asp Ala Ala Ala Met Leu Thr Val Leu Ala Gly Thr Asp Gly	
240 245 250	
ctc gat ccc cga cag acc cac cgg atc gaa ccg gtg gac tac ctc gcg	1897
Leu Asp Pro Arg Gln Thr His Arg Ile Glu Pro Val Asp Tyr Leu Ala	
255 260 265	
gcg ctg gcc gaa ccc gca tcg ggt ctg cgc gtg ggt gtg gtc acc gaa	1945
Ala Leu Ala Glu Pro Ala Ser Gly Leu Arg Val Gly Val Val Thr Glu	
270 275 280	
ggc ttc gac acc cct gtc tcc gac gct gcc gtc gac aat gcc gtg cgc	1993
Gly Phe Asp Thr Pro Val Ser Asp Ala Ala Val Asp Asn Ala Val Arg	
285 290 295 300	
acc gcc atc ggc gta ctg cgc tcg gcc gga ctt acc gtc gaa gag gtc	2041
Thr Ala Ile Gly Val Leu Arg Ser Ala Gly Leu Thr Val Glu Glu Val	
305 310 315	
tcg atc ccc tgg cac ctc gat gcg atg gcc gtc tgg aac gtg atc gac	2089
Ser Ile Pro Trp His Leu Asp Ala Met Ala Val Trp Asn Val Ile Asp	
320 325 330	
cgg gcc gac gac gaa ttc gaa gcc ttc ctg ctg cag gtg ctc gac gag	2137
Arg Ala Asp Asp Glu Phe Glu Ala Phe Leu Leu Gln Val Leu Asp Glu	
335 340 345	
aac gcc gtc acc atc ccc gaa ctc gga cag gtg cgg gcg cag acg ccg	2185
Asn Ala Val Thr Ile Pro Glu Leu Gly Gln Val Arg Ala Gln Thr Pro	
350 355 360	
cgc tcg tgg tgc tca cct cga acc gca ccc gcg agg tgc acg acg ccc	2233
Arg Ser Trp Cys Ser Pro Arg Thr Ala Pro Ala Arg Cys Thr Thr Pro	
365 370 375 380	

tca aac gcc gct gcc tgt acc act ggc tgc aac acc ccg acc tgc cgc	2281
Ser Asn Ala Ala Ala Cys Thr Thr Gly Ser Asn Thr Pro Thr Ser Arg	
385 390 395	
ggg aag tgg aga tcc tgc gcc gcc gca tcc cgg gca tgc acg aac acc	2329
Gly Lys Trp Arg Ser Cys Ala Ala Ala Ser Arg Ala Ser Thr Asn Thr	
400 405 410	
tgc cgg cgc agg tgc ccc acg ccg tgc agg cca tgc gcg gga tgg acc	2377
Ser Arg Arg Arg Ser Pro Thr Pro Cys Arg Pro Cys Ala Gly Trp Thr	
415 420 425	
tgc tca aac cac ccg ggg tgc cgg agt cgc tgg act ggg cac gag cgc	2425
Cys Ser Asn His Pro Gly Ser Arg Ser Arg Trp Thr Gly His Glu Arg	
430 435 440	
tgc ggg aac tgc acc gcg acg tgc tgc acg cga cga ccg cgg ccg cga	2473
Cys Gly Asn Ser Thr Ala Thr Cys Ser Thr Arg Arg Pro Arg Pro Arg	
445 450 455 460	
ccc tgc gtg ccg tcc tga agtaccggga ggacctcgac cgagtgggtcc	2521
Pro Ser Val Pro Ser	
465	
gcaccggggt cgaccgggtc ctgacggggt gacagcggcg atgacgacga ccaccgacgc	2581
cggggggttcc ctgcgtcgac tcaccggctt caccgcgcgc ctgcgcgcgg ccggcctgtc	2641
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Asn His Phe Arg Phe Gly Leu Thr Thr Pro Glu Leu Glu Glu Phe Ala	20	25	30
Pro Ala Leu Glu Ala Thr Leu Ala Ser Ser Glu Thr Val Glu Arg Leu	35	40	45
Tyr Glu Arg Thr Ala Pro Glu Pro Pro Gln Arg Ser Trp Thr Ser Pro	50	55	60
Thr Ala Asp Glu Asn Pro Leu Ser Ala Trp Tyr Val Thr Thr Ser Ile	65	70	75
Ser Glu Thr Asp Glu Gly Pro Leu Ala Gly Arg Thr Val Ala Val Lys	85	90	95
Asp Asn Val Ala Val Ala Gly Val Pro Met Met Asn Gly Ser Arg Thr	100	105	110
Val Glu Gly Phe Thr Pro Arg Tyr Asp Ala Thr Val Val Arg Arg Leu	115	120	125
Leu Asp Ala Gly Ala Thr Ile Thr Gly Lys Ala Val Cys Glu Asp Leu	130	135	140
Cys Phe Ser Gly Ala Ser Phe Thr Ser His Pro Gln Pro Val Arg Asn	145	150	155
Pro Trp Asp Glu Ser Arg Ile Thr Gly Gly Ser Ser Ser Gly Ser Gly	165	170	175
Ala Leu Val Ala Ser Gly Gln Val Asp Met Ala Val Gly Gly Asp Gln	180	185	190
Gly Gly Ser Ile Arg Ile Pro Ala Ala Phe Cys Gly Ile Val Gly His	195	200	205
Lys Pro Thr His Gly Leu Val Pro Tyr Thr Gly Ala Phe Pro Ile Glu	210	215	220
Arg Thr Ile Asp His Leu Gly Pro Met Thr Arg Thr Val Ser Asp Ala	225	230	235
Ala Ala Met Leu Thr Val Leu Ala Gly Thr Asp Gly Leu Asp Pro Arg			

